

**RAW SEQUENCE LISTING
ERROR REPORT**

L. Gansheroff

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/236,995A
Source: 1638
Date Processed by STIC: 11/1/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/236,996A

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213> Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220> Feature (NEW RULES) Sequence(s) ____ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

O:Zagham

1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000

TIME: 13:18:34

Input Set : A:\Polyadpl.app

Output Set: N:\CRF3\11012000\I236995A.raw

Does Not Comply
Corrected Diskette Needed

see 2-9
PP-6-9

3 <110> APPLICANT: Mahajan, Pramod B.
4 Zuo, Zhuang
6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses
8 <130> FILE REFERENCE: 5718-34, 035718-174234
10 <140> CURRENT APPLICATION NUMBER: 09/236,995A
11 <141> CURRENT FILING DATE: 1999-01-26
13 <150> PRIOR APPLICATION NUMBER: 60/072,785
14 <151> PRIOR FILING DATE: 1998-01-27
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2949
22 <212> TYPE: DNA
23 <213> ORGANISM: Zea mays
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(2949)
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (1)..()
32 <223> OTHER INFORMATION: nA, T, C, or G
34 <220> FEATURE:
35 <221> NAME/KEY: misc_feature
36 <222> LOCATION: (1)..(2949)
37 <223> OTHER INFORMATION: Naa-unknown
39 <400> SEQUENCE: 1
40 atg gca gca cca aag gca tga aag gca gat tat gcc aag tct ggg 18
41 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
42 1 5 10 15
44 cag gcc tgc tgc aag tca tgc cga tgc ctt atc gcc aag gac cag ctc 96
45 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
46 20 25 30
48 cgt ctt gcc aag atg gtl cag aag tca cag ttc gac ggc ttc atg ccg 144
49 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
50 35 40 45
52 atg tgg aac cat gcc aag tgc atc ttc agc aag aag aac cag ata aag 192
53 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
54 50 55 60
56 tcc gtt gac gat gtl gaa gga ata gat gca ctt aga tgg gat gat caa 240
57 Ser Val Asp Asp Val Gln Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
58 65 70 75 80
60 gag aag ata cga aac tac gtl gga ggt gcc tca gct ggt aca agt tct 288
61 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
62 85 90 95
64 aca gct gct cct cct gag aag tat aca att gaa att gct cca tct gcc 336
65 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
66 100 105 110

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000

TIME: 13:18:34

Input Set : A:\Polyadpl.app

Output Set: N:\CRF3\11012000\I236995A.raw

68	cgt	act	tca	tgt	aga	cga	tgc	agt	gaa	aag	att	aca	aaa	gga	tcg	gtc	384
69	Arg	Thr	Ser	Cys	Arg	Arg	Cys	Ser	Glu	Lys	Ile	Thr	Lys	Gly	Ser	Val	
70				115			120						125				
72	cgt	ctt	tca	gct	aag	ctt	gag	agt	gaa	ggt	ccc	aag	ggt	ata	cca	tgg	432
73	Arg	Leu	Ser	Ala	Lys	Leu	Glu	Ser	Glu	Gly	Pro	Lys	Gly	Ile	Pro	Trp	
74		130					135						140				
76	tat	cat	gcc	aac	tgt	ttc	ttt	gag	gta	tcc	ccg	tct	gca	act	gtt	gag	480
77	Tyr	His	Ala	Asn	Cys	Phe	Phe	Glu	Val	Ser	Pro	Ser	Ala	Thr	Val	Glu	
78	145					150					155				160		
80	aag	ttc	tca	ggc	tgg	gat	act	tig	ccc	gat	gag	gat	aag	aga	acc	atg	528
81	Lys	Phe	Ser	Gly	Trp	Asp	Thr	Leu	Ser	Asp	Glu	Asp	Lys	Arg	Thr	Met	
82				165						170					175		
84	ctc	gat	ctt	gtt	aaa	aaa	gat	gtt	ggc	aac	aat	gaa	caa	aat	aag	ggt	576
85	Leu	Asp	Leu	Val	Lys	Lys	Asp	Val	Gly	Asn	Asn	Glu	Gln	Asn	Lys	Gly	
86				180					185						190		
88	tcc	aag	cgc	aag	aaa	agt	gaa	aat	gat	att	gat	agc	tac	aaa	tcc	ccc	624
89	Ser	Lys	Arg	Lys	Lys	Ser	Glu	Asn	Asp	Ile	Asp	Ser	Tyr	Lys	Ser	Ala	
90		195					200				205						
92	agg	tta	gat	gaa	agt	aca	tct	gaa	ggt	aca	gtg	cga	aac	aaa	ggg	caa	672
93	Arg	Leu	Asp	Glu	Ser	Thr	Ser	Glu	Gly	Thr	Val	Arg	Asn	Lys	Gly	Gln	
94		210					215				220						
96	ctt	gta	gac	cca	cgt	ggt	tcc	aat	act	agt	tca	gct	gat	atc	caa	cta	720
97	Leu	Val	Asp	Pro	Arg	Gly	Ser	Asn	Thr	Ser	Ser	Ala	Asp	Ile	Gln	Leu	
98	225					230					235				240		
100	aag	ctt	aaa	gag	caa	aat	gac	aca	ctt	tgg	aaq	tta	aaq	gat	gga	ctt	768
101	Lys	Leu	Lys	Gln	Gln	Ser	Asp	Thr	Leu	Trp	Lys	Leu	Lys	Asp	Gly	Leu	
102				245						250					255		
104	aag	act	cat	gta	tcc	gct	gct	gaa	tta	agg	gat	atg	ctt	gag	gct	aat	816
105	Lys	Thr	His	Val	Ser	Ala	Ala	Glu	Leu	Arg	Asp	Met	Leu	Glu	Ala	Asn	
106				260					265					270			
108	gag	caq	gat	aca	tca	gga	cca	gaa	agg	cac	cta	ttg	gat	cgc	tgt	gcg	864
109	Gly	Gln	Asp	Thr	Ser	Gly	Pro	Glu	Arg	His	Leu	Leu	Asp	Arg	Cys	Ala	
110		275					280				285						
112	gat	gga	atg	cta	tat	gga	gag	ctg	ggt	ccc	tgc	cca	gtc	tgt	gct	aat	912
113	Asp	Gly	Met	Leu	Phe	Gly	Ala	Leu	Gly	Pro	Cys	Pro	Val	Cys	Ala	Asn	
114		290					295				300						
116	ggc	atg	tac	tat	tat	aat	ggt	caq	tac	caa	tgc	agt	ggt	aat	gtg	tca	960
117	Gly	Met	Tyr	Tyr	Tyr	Asn	Gly	Gln	Tyr	Gln	Cys	Ser	Gly	Asn	Val	Ser	
118	305					310					315				320		
120	gag	tgg	tcc	aaq	tgt	aca	tac	tct	ccc	aca	gaa	ccc	gtc	cac	gtt	aaq	1008
121	Glu	Trp	Ser	Lys	Cys	Thr	Lys	Ser	Ala	Thr	Glu	Pro	Val	Arg	Val	Lys	
122				325						330					335		
124	aaq	aag	tgg	caa	att	cca	cat	gga	aca	aaq	aat	gat	tac	ctt	atg	aaq	1056
125	Lys	Lys	Trp	Gln	Ile	Pro	His	Gly	Thr	Lys	Asn	Asp	Tyr	Leu	Met	Lys	
126				340					345					350			
128	tgg	ttc	aaa	tct	caa	aaq	gtt	aaq	aaa	cca	gag	agg	gtt	ctt	cca	cca	1104
129	Trp	Phe	Lys	Ser	Gln	Lys	Val	Lys	Lys	Pro	Glu	Arg	Val	Leu	Pro	Pro	
130				355			360				365						
132	atg	tca	ccc	gag	aaa	tct	gga	agt	aaa	gca	act	cag	aga	aca	tca	ttg	1152

RAW SEQUENCE LISTING

DATE: 11/01/2000

PATENT APPLICATION: US/09/236,995A

TIME: 13:18:34

Input Set : A:\Polyadpl.app

Output Set : N:\CRF3\11012000\I236995A.raw

```

133 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
134 370 375 380
136 ctg tct tct aaa qgg ttg gat aaa tta agg ttt tct gtt gta gga caa 1200
137 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
138 385 390 395 400
140 tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt 1248
141 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
142 405 410 415
144 gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca 1296
145 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
146 420 425 430
148 tat gat gag ctc gac aat gaa aat gct gaa gtc agg aaa gca agg agg 1344
149 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
150 435 440 445
152 ctg aag ata cca att gta agg gag gat tac att gga gaa tgt gtt aaa 1392
153 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
154 450 455 460
156 aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag 1440
157 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
158 465 470 475 480
160 tcc tca aaa gcc mgt act gtc act gtt aaa gtt aag gcc cga aqt gct 1488
W--> 161 Ser Ser Lys Gly Xaa Thr Val Lys Val Lys Gly Arg Ser Ala
162 485 490 495
164 tat tca tta aat act cct cgg gtt tgc aag aat act gct cac att cct tra 1536
W--> 165 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
166 500 505 510
168 gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn 1584
W--> 169 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
170 515 520 525
172 cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat 1632
W--> 173 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
174 530 535 540
176 gat qgg tct aag tgc tac gta ttt cgt aag tgg gga cgg gtt qgg aat 1680
177 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
178 545 550 555 560
180 gga aaa att qga qgg cca aaa ctg gag gag atg tca aaa act gag gca 1728
181 Gln Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
182 565 570 575
184 atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg 1776
185 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
186 580 585 590
188 gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct qgg aga ttt 1824
189 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
190 595 600 605
192 tcc cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aat 1872
193 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
194 610 615 620
196 gat aac aat gaa atg aaa aat tct ctt gct cct caa ttg cta gaa ctc 1920
197 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000

TIME: 13:18:34

Input Set: A:\Polyadpl.app

Output Set: N:\CRF3\11012000\I236995A.raw

198	625	630	635	640	
200	atg aag atg ctt ttc aat gtg gag aca tat aga gct gct atg atg gaa	1968			
201	Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu				
202	645	650	655		
204	ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra	2016			
W--> 205	Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa				
206	660	665	670		
208	aat att gag raa gga ttt gaa gca tta act krg rta cmq rat tta ttt	2064			
W--> 209	Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe				
210	675	680	685		
W--> 212	gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg	2112			
W--> 213	Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu				
214	690	695	700		
216	ttg ttg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc	2160			
W--> 217	Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu				
218	705	710	715	720	
220	ata tta tac ggg atg agg atg att tca tat tca baq gcq aaa atq ctt	2208			
221	Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu				
222	725	730	735		
224	gaa gct ctg caq qat att gaa att gct tca aag ata gtt agc ttc qat	2256			
225	Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp				
226	740	745	750		
228	agc qac agt gat gaa tct ctt gat gat aac tat atq aaa ctt cgc tqt	2304			
229	Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys				
230	755	760	765		
232	gac atc acc ccg ctg gct cac gat agt gaa gtt tac aag tta att gaa	2352			
233	Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu				
234	770	775	780		
236	caq tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcc ctg	2400			
237	Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu				
238	785	790	795	800	
240	gaa ctg qag gaa gtt ttt tca ctt gat cga gat aag gaa ctt aat aag	2448			
241	Glu Leu Gln Glu Val Phe Ser Leu Asp Arg Asp Gly Gln Leu Asn Lys				
242	805	810	815		
244	tac tca aga tat aca aat aat ctg cat aac aag atq cta tta tgg cac	2496			
245	Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His				
246	820	825	830		
248	ggt tca agg ttg acg aat ttt gtg gga att ctt agt aag ggg cta aag	2544			
249	Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg				
250	835	840	845		
252	att aca cct cct gag gca cct gtt act ggc tat atg ttc ggc aac ggc	2592			
253	Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly				
254	850	855	860		
256	ctc tac ttt gca gat cta gta agc aag aag aca cca tac tgt tat gta	2640			
257	Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val				
258	865	870	875	880	
260	gat aag aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta	2688			
261	Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu				
262	885	890	895		

RAW SEQUENCE LISTING

DATE: 11/01/2000

PATENT APPLICATION: US/09/236,995A

TIME: 13:18:34

Input Set : A:\Polyadpl.app

Output Set: N:\CRF3\11012000\I236995A.raw

```

264 gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca 2736
265 Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro
266 900 905 910
268 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784
269 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
270 915 920 925
272 tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
273 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
274 930 935 940
276 ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac 2880
277 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
278 945 950 955
280 atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg 2928
281 Ile Val Tyr Asn Thr Ser Glu Val Lys Met Glu Phe Leu Leu Lys Val
282 965 970 975
284 cgt ttc cat cac aag aag tag 2949
285 Arg Phe His His Lys Arg
286 980
289 <210> SEQ ID NO: 2
290 <211> LENGTH: 982
291 <212> TYPE: PRT
292 <213> ORGANISM: Tet. aays
294 <400> SEQUENCE: 2
295 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
296 1 5 10 15
297 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Glu Leu
298 20 25 30
299 Arg Leu Gly Lys Met Val Glu Ala Ser Glu Phe Asp Gly Phe Met Pro
300 35 40 45
301 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Glu Ile Lys
302 50 55 60
303 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Glu
304 65 70 75 80
305 Glu Lys Ile Arg Asn Trp Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
306 85 90 95
307 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
308 100 105 110
309 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
310 115 120 125
311 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
312 130 135 140
313 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
314 145 150 155 160
315 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
316 165 170 175
317 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Glu Asn Lys Gly
318 180 185 190
319 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
320 195 200 205

```

see pp 6-7

<210> 2
 <211> 982
 <212> PRT
 <213> Zea mays

see next page

<400> 2
 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly
 1 5 10 15
 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
 20 25 30
 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
 35 40 45
 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
 50 55 60
 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
 65 70 75 80
 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 85 90 95
 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 100 105 110
 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 115 120 125
 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
 130 135 140
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 145 150 155 160
 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 165 170 175
 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
 180 185 190
 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 195 200 205
 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
 210 215 220
 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 225 230 235 240
 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 245 250 255
 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
 260 265 270
 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
 275 280 285
 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
 290 295 300
 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
 305 310 315 320
 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335
 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350
 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly

09/23/99

9

405	410	415
Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala		
420	425	430
Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg		
435	440	445
Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys,		
450	455	460
Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu		
465	470	475
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala		
485	490	495
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa		
500	505	510
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa		
515	520	525
His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp		
530	535	540
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser		
545	550	555
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala		
565	570	575
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp		
580	585	590
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe		
595	600	605
Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys		
610	615	620
Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu		
625	630	635
Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu		
645	650	655
Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa		
660	665	670
Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe		
675	680	685
Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu		
690	695	700
Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu		
705	710	715
Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu		
725	730	735
Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp		
740	745	750
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys		
755	760	765
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu		
770	775	780
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu		
785	790	795
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys		
805	810	815
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His		
820	825	830
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg		
835	840	845
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly		
850	855	860

See
item 10
on Enw
summary
sheet

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000
TIME: 13:18:35

Input Set : A:\Polyadpl.app
Output Set : N:\CRF3\11012000\I236995A.raw

L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:355 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:355 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:355 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:355 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
M:340 Repeated in SeqNo=2
L:359 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:359 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2